RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/576,528
Source: IFW
Date Processed by STIC: 5/1/06

ENTERED

IFWP

RAW SEQUENCE LISTING DATE: 05/01/2006
PATENT APPLICATION: **US/10/576,528** TIME: 10:51:53

Input Set : **A:\CRF4 SQ Listing-19 Apr 2006.txt**
Output Set: **N:\CRF4\05012006\J576528.raw**

```
      3 <110> APPLICANT: Schnorr, Kirk Matthew
      4       Christensen, Lars Lehmann Hylling
      6 <120> TITLE OF INVENTION: Fungal carbohydrate-binding module
      8 <130> FILE REFERENCE: 10499.204-US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/576,528
C--> 10 <141> CURRENT FILING DATE: 2006-04-19
     10 <160> NUMBER OF SEQ ID NOS: 9
     12 <170> SOFTWARE: PatentIn version 3.3
     14 <210> SEQ ID NO: 1
     15 <211> LENGTH: 529
     16 <212> TYPE: DNA
     17 <213> ORGANISM: Pseudoplectania nigrella
     20 <220> FEATURE:
     21 <221> NAME/KEY: CDS
     22 <222> LOCATION: (10)..(531)
     24 <400> SEQUENCE: 1
     25 gaattcaaa atg gtc aac ttc acc acc ctc ctc ccg gtt ctt gcc gct ctt     51
     26           Met Val Asn Phe Thr Thr Leu Leu Pro Val Leu Ala Ala Leu
     27           1               5                   10
     29 att gga gct gcc aat gcc cac act cgt gtc tac gga ctc tcc gtc aac      99
     30 Ile Gly Ala Ala Asn Ala His Thr Arg Val Tyr Gly Leu Ser Val Asn
     31 15                  20                  25                  30
     33 gat gtc aca tcc tcc ggc acc tcc aat gac aag gcc gtc gct tct tcc     147
     34 Asp Val Thr Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser
     35                 35                  40                  45
     37 agt att gcg gcc gtg gac cct gtg acc agc tcc gtc gta gcc tct gtt     195
     38 Ser Ile Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val
     39             50                  55                  60
     41 cag gtc cct aac ttc act gcc act gac gtc ccc act ttt act gcc acc     243
     42 Gln Val Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr
     43         65                  70                  75
     45 gac atc cct act ttc act gct act gat gtt cct atc ttc acc aag aag     291
     46 Asp Ile Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys
     47     80                  85                  90
     49 ccc caa cag ccc tca act tta ttg acc cgc acc cgt acc cat gcc tct     339
     50 Pro Gln Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser
     51 95                  100                 105                 110
     53 gtt tca ttc gtc gct aag ccc tcc gct ttt att ccc aag cct tcc gcg     387
     54 Val Ser Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala
     55                 115                 120                 125
     57 agc aca atc ccg tca aag ccc aag act ccc gaa gag gtt aat aag tgc     435
     58 Ser Thr Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys
     59             130                 135                 140
```

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```
 61 ctt gac gct gtc aac gcc tgt att aca cag gcc cag agc tcc att gga      483
 62 Leu Asp Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly
 63         145                 150                 155
 65 gga gtt gtc aac ttt gag cct tgc gag agc cag aga gct ctt tgc tat      531
 66 Gly Val Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
 67     160                 165                 170
 69 taggaactgc aaagaatctg gggggatggt agcgaggttg agaggtggag gagcggaggc     591
 71 gtaggggagg tgagatggag taagattaag cggccgca                           629
 74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 174
 76 <212> TYPE: PRT
 77 <213> ORGANISM: Pseudoplectania nigrella
 79 <400> SEQUENCE: 2
 81 Met Val Asn Phe Thr Thr Leu Leu Pro Val Leu Ala Ala Leu Ile Gly
 82 1               5                  10                  15
 85 Ala Ala Asn Ala His Thr Arg Val Tyr Gly Leu Ser Val Asn Asp Val
 86             20                  25                  30
 89 Thr Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile
 90         35                  40                  45
 93 Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val
 94     50                  55                  60
 97 Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile
 98 65                  70                  75                  80
101 Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln
102                 85                  90                  95
105 Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser
106             100                 105                 110
109 Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr
110         115                 120                 125
113 Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp
114     130                 135                 140
117 Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val
118 145                 150                 155                 160
121 Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
122                 165                 170
125 <210> SEQ ID NO: 3
126 <211> LENGTH: 31
127 <212> TYPE: DNA
128 <213> ORGANISM: Pseudoplectania nigrella
131 <220> FEATURE:
W--> 132 <221> NAME/KEY: misc_feature Primer NP887U1
133 <222> LOCATION: (1)..(31)
135 <400> SEQUENCE: 3
136 gacatcgttg acggagagtc cgtagacacg a                                    31
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 34
141 <212> TYPE: DNA
142 <213> ORGANISM: Pseudoplectania nigrella
145 <220> FEATURE:
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Input Set : **A:\01-SQ Listing-19 Apr 2006.txt**
Output Set: **N:\CRF4\05012006\J576528.raw**

W--> 146 <221> NAME/KEY: misc_feature Primer NP887D1
147 <222> LOCATION: (1)..(34)
149 <400> SEQUENCE: 4
150 acatcctccg gcacctccaa tgacaaggcc gtcg 34
153 <210> SEQ ID NO: 5
154 <211> LENGTH: 21
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Primer PNA2I
162 <220> FEATURE:
W--> 163 <221> NAME/KEY: misc_feature Primer PNA2I
164 <222> LOCATION: (1)..(21)
166 <400> SEQUENCE: 5
167 gtttccaact caatttacct c 21
170 <210> SEQ ID NO: 6
171 <211> LENGTH: 32
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Primer NP887Dau1
179 <220> FEATURE:
W--> 180 <221> NAME/KEY: misc_feature Primer NP887Dau1
181 <222> LOCATION: (1)..(32)
183 <400> SEQUENCE: 6
184 ccaaagcttt tcatcctccg gcacctccaa tg 32
187 <210> SEQ ID NO: 7
188 <211> LENGTH: 32
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Primer N887Dau2
196 <220> FEATURE:
W--> 197 <221> NAME/KEY: misc_feature Primer NP887Dau2
198 <222> LOCATION: (1)..(32)
200 <400> SEQUENCE: 7
201 gcgaagctta atcttactcc atctcacctc cc 32
204 <210> SEQ ID NO: 8
205 <211> LENGTH: 573
206 <212> TYPE: DNA
207 <213> ORGANISM: Pseudoplectania nigrella
210 <220> FEATURE:
211 <221> NAME/KEY: CDS
212 <222> LOCATION: (1)..(570)
213 <223> OTHER INFORMATION: Positions 1-57 Candida lipase signal peptide, positions 58-147
214 Candida lipase sequence, positions 148-570 P. nigrella CBM
215 polypeptide.
217 <400> SEQUENCE: 8
218 atg aag cta ctc tct ctg acc ggt gtg gct ggt gtg ctt gcg act tgc 48

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```
219 Met Lys Leu Leu Ser Leu Thr Gly Val Ala Gly Val Leu Ala Thr Cys
220 1               5                   10                  15
222 gtt gca gcc act cct ttg gtg aag tgc gca act agt ggc cat tac ggc      96
223 Val Ala Ala Thr Pro Leu Val Lys Cys Ala Thr Ser Gly His Tyr Gly
224             20                  25                  30
226 ctc gcg agg ccg cct cgg ccc caa cga att ctt gga ata tta agc ttt     144
227 Leu Ala Arg Pro Pro Arg Pro Gln Arg Ile Leu Gly Ile Leu Ser Phe
228         35                  40                  45
230 tca tcc tcc ggc acc tcc aat gac aag gcc gtc gct tct tcc agt att     192
231 Ser Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile
232     50                  55                  60
234 gcg gcc gtg gac cct gtg acc agc tcc gtc gta gcc tct gtt cag gtc     240
235 Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val
236 65                  70                  75                  80
238 cct aac ttc act gcc act gac gtc ccc act ttt act gcc acc gac atc     288
239 Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile
240                 85                  90                  95
242 cct act ttc act gct act gat gtt cct atc ttc acc aag aag ccc caa     336
243 Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln
244             100                 105                 110
246 cag ccc tca act tta ttg acc cgc acc cgt acc cat gcc tct gtt tca     384
247 Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser
248         115                 120                 125
250 ttc gtc gct aag ccc tcc gct ttt att ccc aag cct tcc gcg agc aca     432
251 Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr
252     130                 135                 140
254 atc ccg tca aag ccc aag act ccc gaa gag gtt aat aag tgc ctt gac     480
255 Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp
256 145                 150                 155                 160
258 gct gtc aac gcc tgt att aca cag gcc cag agc tcc att gga gga gtt     528
259 Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val
260                 165                 170                 175
262 gtc aac ttt gag cct tgc gag agc cag aga gct ctt tgc tat tag         573
263 Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
264             180                 185                 190
267 <210> SEQ ID NO: 9
268 <211> LENGTH: 190
269 <212> TYPE: PRT
270 <213> ORGANISM: Pseudoplectania nigrella
272 <400> SEQUENCE: 9
274 Met Lys Leu Leu Ser Leu Thr Gly Val Ala Gly Val Leu Ala Thr Cys
275 1               5                   10                  15
278 Val Ala Ala Thr Pro Leu Val Lys Cys Ala Thr Ser Gly His Tyr Gly
279             20                  25                  30
282 Leu Ala Arg Pro Pro Arg Pro Gln Arg Ile Leu Gly Ile Leu Ser Phe
283         35                  40                  45
286 Ser Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile
287     50                  55                  60
290 Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val
```

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Output Set: **N:\CRF4\05012006\J576528.raw**

```
291 65                  70                  75                  80
294 Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile
295                 85                  90                  95
298 Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln
299             100                 105                 110
302 Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser
303         115                 120                 125
306 Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr
307     130                 135                 140
310 Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp
311 145                 150                 155                 160
314 Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val
315                 165                 170                 175
318 Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr
319             180                 185                 190
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/01/2006
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Input Set : **A:\01-SQ Listing-19 Apr 2006.txt**
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7

VERIFICATION SUMMARY DATE: 05/01/2006
PATENT APPLICATION: **US/10/576,528** TIME: 10:51:54

Input Set : **A:\01-SQ Listing-19 Apr 2006.txt**
Output Set: **N:\CRF4\05012006\J576528.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:132 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:146 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:163 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:180 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7